Amendments to the Claim:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1 (currently amended). A pharmaceutical composition comprising an apolipoprotein protein construct having the general formula

- apo-A-X,

- where apo-A is an apolipoprotein component selected from the group consisting of apolipoprotein A-I, apolipoprotein A-II, and apolipoprotein A-IV~~, a functional analogue or variant thereof~~,

- and X is a tetranectin trimerising module ~~heterologous moiety comprising at least one compound selected from the group consisting of an amino acid, a peptide, a protein, a carbohydrate, and a nucleic acid sequence,~~

~~- with the proviso that when the construct consists of exactly two identical, native apolipoproteins these are linked serially~~.

2 (currently amended). The composition of claim 1, further comprising a spacer peptide between the apo-A component and the tetranectin trimerising module~~X~~, wherein the spacer peptide comprises ~~a spacer peptide comprising~~ at least two amino acids.

3 (currently amended). The composition according to claim 2, wherein the spacer peptide is essentially non-immunogenic, and/or is not prone to proteolytic cleavage and/or does not comprise any cystein residues.

4 (currently amended). The composition according to claim 2, wherein the three-dimensional structure of the spacer is linear ~~or substantially linear~~.

5 (currently amended). The composition according to claim 2, wherein the spacer peptide comprises an ~~the~~ amino acid sequence selected from the group consisting of GTKVHMK (SEQ ID NO:69) ~~from tetranectin, amino acid sequence~~ PGTSGQQPSVGQQ (SEQ ID NO:70), ~~and~~ GTSGQ (residues 2-6 of SEQ ID NO:70) ~~from the connecting strand 3 from human fibronectin~~, PKPSTPPGSS (SEQ ID NO:71) ~~from the upper hinge region of murine IgG$_3$~~, SGGTSGSTSGTGST (SEQ ID NO:72), AGSSTGSSTGPGSTT (SEQ ID NO:73) ~~or~~ and GGSGGAP (SEQ ID NO:74).

6 (currently amended). The composition of claim 1, wherein the tetranectin trimerising module ~~component X~~ is linked by a covalent link to the N-terminal or the C-terminal amino acid of apo-A.

7-21 (cancelled).

22 (currently amended). The composition of claim ~~1~~21, wherein the tetranectin trimerising module is part of ~~capable of forming~~ a stable trimeric complex with two other tetranectin trimerising modules.

23 (currently amended). The composition of ~~the~~ claim~~s~~ 22, wherein the stable trimeric complex includes a coiled coil structure.

24 (currently amended). The composition of claim 23, wherein the coiled coil structure is a triple alpha helical coiled coil.

25 (currently amended). The composition of ~~the~~ claim 22~~21~~, wherein the stable trimeric complex ~~trimerising module~~ comprises two tetranectin trimerising modules linked by a spacer moiety, which allows both of the two tetranectin trimerising modules to take part in the~~a~~ complex formation with a third tetranectin trimerising module not being part of the apolipoprotein protein construct.

26 (currently amended). The composition of ~~the~~ claim~~s~~ 1~~21~~, wherein ~~at least one~~ the tetranectin trimerising module is selected from the group consisting of human tetranectin, murine tetranectin or C-type lectin of human, bovine or shark cartilage.

27 (currently amended). The composition of ~~the~~ claim~~s~~ 1~~21~~, wherein the tetranectin trimerising module comprises a sequence having at least 68% identity with the sequence of SEQ ID NO 12 and is capable of forming a stable trimeric complex with other tetranectin trimerising modules.

28 (currently amended). The composition of claim 27, wherein the cysteine residue ~~no.~~ 50 in SEQ ID NO 12 is

substituted by a serine residue, a threonine residue, or a methionine residue.

29 (currently amended). The composition of claim 1~~16~~, wherein the tetranectin trimerisation module has at least 68% sequence identity with the Trip A module (SEQ ID NO 13) and is capable of forming a stable trimeric complex with other tetranectin trimerising modules..

30-31 (cancelled).

32 (currently amended). The composition of claim 22~~1~~, wherein the stable trimeric complex has ~~having~~ a half-life at least 2 times the half-life of native apolipoprotein~~Apo~~ A-I, A-II or A-IV.

33 (currently amended). The composition of claim 22~~1~~, wherein said stable trimeric complex is capable of binding to a receptor or protein selected from the group consisting of cubilin, megalin, Scavenger receptor class B, type 1 (SR-B1), ATP-binding cassette 1 (ABC1), Lecithin:cholesterol acyltransferase (LCAT), Cholesteryl-ester transfer protein (CETP), and Phospolipid transfer protein (PLTP).

34 (cancelled).

35 (currently amended). The composition according to claim ~~1~~33, wherein the trimeric complex comprises ~~having~~ an amino acid sequence having ~~of sharing~~ at least 70% sequence identity to one of the sequences SEQ ID NO 2, SEQ ID NO 3,

SEQ ID NO 4, SEQ ID NO 5, SEQ ID NO 6, SEQ ID NO 7, SEQ ID NO 8, SEQ ID NO 9, SEQ ID NO 10 or SEQ ID NO 11 ~~to SEQ ID NO 11, or SEQ ID NO 14~~.

36 (cancelled).

37 (currently amended). The composition of claim 1, further comprising pharmaceutical acceptable excipients, adjuvants, or additives.

38 (currently amended). An apolipoprotein protein construct having the general formula

- apo-A-X,

- where apo-A is an apolipoprotein component selected from the group consisting of apolipoprotein A-I, apolipoprotein A-II, and apolipoprotein A-IV, ~~an functional analogue or variant thereof,~~

- and X is a tetranectin trimerising module ~~heterologous moiety selected from the group consisting of an oligomerising module, and a terminally linked apolipoprotein.~~

39 (currently amended). The construct of claim 38, further comprising a spacer peptide between the apo-A component and the tetranectin trimerising module~~X~~, wherein the spacer peptide comprises at least two amino acids.

40 (currently amended). The construct according to claim

39, wherein the spacer peptide is essentially non-immunogenic, and/or is not prone to proteolytic cleavage and/or does not comprise any cysteine residues.

41 (currently amended). The construct according to claim 39, wherein the three-dimensional structure of the spacer peptide is linear ~~or substantially linear~~.

42 (currently amended). The construct according to claim 39, wherein the spacer peptide comprises an ~~the~~ amino acid sequence selected from the group consisting of GTKVHMK (SEQ ID NO:69) ~~from tetranectin~~, ~~amino acid sequence~~ PGTSGQQPSVGQQ (SEQ ID NO:70), ~~and~~ GTSGQ (residues 2-6 of SEQ ID NO:70) ~~from the connecting strand 3 from human fibronectin~~, PKPSTPPGSS (SEQ ID NO:71) ~~from the upper hinge region of murine IgG$_3$~~, SGGTSGSTSGTGST (SEQ ID NO:72), AGSSTGSSTGPGSTT (SEQ ID NO:73) ~~or~~ and GGSGGAP (SEQ ID NO:74).

43-51 (cancelled).

52 (currently amended). The construct of claim 38~~51~~, wherein the tetranectin trimerising module is part of ~~capable of forming~~ a stable trimeric complex with two other tetranectin trimerising modules.

53 (currently amended). The construct of ~~the~~ claim~~s~~ 52, wherein the stable complex comprises a coiled coil structure.

54 (original). The construct of claim 53, wherein the

coiled coil structure is a triple alpha helical coiled coil.

55 (currently amended). The construct of ~~the~~ claim~~s~~ 52~~51~~, wherein the stable trimeric complex ~~trimerising module~~ comprise~~s~~~~ing~~ two tetranectin trimerising modules linked by a spacer moiety, which allows both of the two tetranectin trimerising modules to take part in the~~a~~ complex formation with a third tetranectin trimerising module not being part of the apolipoprotein protein construct.

56 (currently amended). The construct of ~~the~~ claim~~s~~ 52~~51~~, wherein ~~at least one~~ the tetranectin trimerising module is selected from the group consisting of human tetranectin, murine tetranectin or C-type lectin of human, bovine or shark cartilage.

57 (currently amended). The construct of ~~the~~ claim~~s~~ 52~~51~~, wherein the tetranectin trimerising module comprises a sequence having at least 68% sequence identity with the sequence of SEQ ID NO 12 and is capable of forming a stable trimeric complex with other tetranectin trimerising modules.

58 (currently amended). The construct of claim 57, wherein the cysteine residue ~~no.~~ 50 in SEQ ID NO 12 is substituted by a serine residue, a threonine residue, or a methionine residue.

59 (currently amended). The construct of claim 52~~47~~, wherein the tetranectin ~~trimerisation~~ trimerising module

has at least 68% sequence identity with the Trip A module (SEQ ID NO 13) and is capable of forming a stable trimeric complex with other tetranectin trimerising modules.

60-61 (cancelled).

62 (currently amended). The construct according to claim 103~~38~~, wherein the trimeric complex comprises~~ing~~ an amino acid sequence having at least 70% sequence identity to at least one of the sequences SEQ ID NO 3, SEQ ID NO 4, SEQ ID NO 5, SEQ ID NO 6, SEQ ID NO 7, SEQ ID NO 8, SEQ ID NO 9, SEQ ID NO 10 ~~-~~or ~~to~~ SEQ ID NO 11~~, or SEQ ID NO 14~~.

63-84 (cancelled).

85 (new). The composition of claim 22, wherein the stable trimeric complex has a half-life at least 3 times the half-life of native apolipoprotein A-I, A-II or A-IV.

86 (new). The composition of claim 22, wherein the stable trimeric complex has a half-life at least 4 times the half-life of native apolipoprotein A-I, A-II or A-IV.

87 (new). The composition of claim 22, wherein the stable trimeric complex has a half-life at least 10 times the half-life of native apolipoprotein A-I, A-II or A-IV.

88 (new). The composition of claim 1, wherein the apolipoprotein A-I is human apolipoprotein A-I.

89 (new). The composition of claim 1, wherein the

apolipoprotein A-I is a fragment of human apolipoprotein A-I.

90 (new). The composition of claim 89, wherein the fragment of human apolipoprotein A-I comprises at least the amino acids 100-186 of human apolipoprotein A-I.

91 (new). The composition of claim 89, wherein the fragment of human apolipoprotein A-I comprises at least the amino acids 25-267 of human apolipoprotein A-I (SEQ ID NO 1).

92 (new). The composition of claim 89, wherein the fragment of human apolipoprotein A-I is amino acids no 68-267 from human apolipoprotein A-I.

93 (new). The construct according to claim 38, wherein the tetranectin trimerising module is linked by a covalent link to the N-terminal or the C-terminal amino acid of apo-A.

94 (new). The construct of claim 52, wherein the stable trimeric complex has a half-life at least 2 times the half-life of native apolipoprotein A-I, A-II or A-IV.

95 (new). The construct of claim 52, wherein the stable trimeric complex has a half-life at least 3 times the half-life of native apolipoprotein A-I, A-II or A-IV.

96 (new). The construct of claim 52, wherein the stable trimeric complex has a half-life at least 4 times the half-life of native apolipoprotein A-I, A-II or A-IV.

97 (new). The construct of claim 52, wherein the stable trimeric complex has a half-life at least 10 times the half-life of native apolipoprotein A-I, A-II or A-IV.

98 (new). The construct of claim 38, wherein the apolipoprotein A-I is human apolipoprotein A-I.

99 (new). The construct of claim 38, wherein the apolipoprotein A-I is a fragment of human apolipoprotein A-I.

100 (new). The construct of claim 99, wherein the fragment of human apolipoprotein A-I comprises at least the amino acids 100-186 of human apolipoprotein A-I.

101 (new). The construct of claim 99, wherein the fragment of human apolipoprotein A-I comprises at least the amino acids 25-267 of human apolipoprotein A-I (SEQ ID NO 1).

102 (new). The construct of claim 99, wherein the fragment of human apolipoprotein A-I is amino acids no 68-267 from human apolipoprotein A-I.

103 (new). The construct of claim 52, wherein said stable trimeric complex is capable of binding to a receptor or protein selected from the group consisting of cubilin, megalin, Scavenger receptor class B, type 1 (SR-B1), ATP-binding cassette 1 (ABC1), Lecithin:cholesterol acyltransferase (LCAT), Cholesteryl-ester transfer protein (CETP), and Phospolipid transfer protein (PLTP).

104 (new). A trimeric complex comprising an apolipoprotein protein construct having the general formula apo-A-X, where apo-A is an apolipoprotein component selected from the group consisting of apolipoprotein A-I, apolipoprotein A-II, and apolipoprotein A-IV, and X is a tetranectin trimerising module.